



## SEQUENCE LISTING

<110> HONG, GUO FAN  
HUANG, WEI-HUA

<120> DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE  
SELECTIVE DISCRIMINATION AGAINST FLUORESCENT  
DYE-LABELED DIDEOXYNUCLEOTIDES

<130> Lee109

<140> 09/512,019  
<141> 2000-02-24

<150> 09/157,397  
<151> 1998-09-12

<150> 08/642,684  
<151> 1996-05-03

<160> 16

<170> PatentIn Ver. 3.2

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<213> *Bacillus stearothermophilus*

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<213> *Bacillus stearothermophilus*

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Leu Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu  
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Ala Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys  
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Ser Met Phe Asp Ala Lys Arg Ala Val Val Ala Leu Lys Trp Lys Gly  
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Ile Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu  
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Leu Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met  
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Lys Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly  
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Val Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val  
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Arg Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp  
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Leu Arg Asn Asn Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu His Ala  
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Leu Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp  
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Thr Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg  
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Ala Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile  
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Asn Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu  
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Pro Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val  
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Leu Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His  
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Tyr Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu  
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Lys Val Val Arg Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln  
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Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln  
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 Ala Lys Ala Val Asn Tyr Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly  
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tatcagggcg atggccacta cgtgaaccat cacccaaatc aagtttttg gggtcgaggt 600  
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<223> a, c, g, t, other or unknown

<220>
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<222> (384)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (387)
<223> a, c, g, t, other or unknown

<220>
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<222> (389)
<223> a, c, g, t, other or unknown

<220>
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<223> a, c, g, t, other or unknown

<220>
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<222> (404)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (446)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (467)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (490)
<223> a, c, g, t, other or unknown
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<220>
<221> modified_base
<222> (563)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (590)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (597)
<223> a, c, g, t, other or unknown

<400> 14
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agntgtttcc tggtaatccgn tcacaattcc acanaaaata cgngncgggn 180
gnataaagtg taaagcctgg ggtgncta at gngtngtta antcacatta attgngttgn 240
gntcaatgnc cgnttccag tcgggnnaacc tggcgtgnca gntgnattaa tggttcggcc 300
aacgngccgg gngngnggt ttgggtattt gngntcttc cgnttccctcg ntcantgatt 360
cggtgnntc ggtcggtccg ntgngngng ngttacatcaga tcantcaaag gggtaatac 420
ggttattccac agaatcaggg gtaanggag gtaaggacat gtgggnnaaa agggcagcaa 480
aaggccaggn accgtaaaaaa ggccgggttgg ttgggtttt tccatagggt cccggccct 540
gggggggatc aaaaaaaaaatc cgngccaaag tcaagggggtg gggggaccn ccagggnnta 600
taaaggtaacc aggggttccc cctggagtc cctccgtggg tctcctgtcc gccctgccc 660
ttacccgta ct 672

<210> 15
<211> 686
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Template DNA
      sequence

<220>
<221> modified_base
<222> (561)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (656)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (678)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (680)
<223> a, c, g, t, other or unknown

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<221> modified_base
<222> (682)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (685)
<223> a, c, g, t, other or unknown

<400> 15
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acaattccac acaacatacg agccggaaagc ataaaagtgtt aaggcctgggg tgccaatgag 120
tgagcttaact cacattaatt gcgttgcgtt cactgcccgc tttccagtcg gaaaacctgt 180
cgtgcagct gcattaatga atcggccaac ggcggggag aggcggttt cgtattggc 240
gccagggtgg tttttctttt caccagttag acgggcaaca gctggattgc ctttcaccgc 300
ctggccctga gagagttgca gcaagcggtc cacgctgggt tgccccagca ggcgaaaatc 360
ctgtttgatg gtggttccga aatcgccaaa atcccttata aatcaaaaga ataggccgag 420
atagggttga gtgttgttcc agtttgaac aagagtccac tattaaagaa cgtggactcc 480
aacgtcaaaag ggcgaaaac cgtctatcag ggcgatgcca ctacgtgaac catcacccaa 540
atcaagttt ttggggtcga ngttgcgtt aagcattaaa tcggaaacct aaagggagcc 600
ccgattttaga gcttgagggg gaaagccggc gaacgtggc gagaaaaagg aggggnagaa 660
accgaaagga gcccctnan gncngn 686

<210> 16
<211> 673
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Template DNA
      sequence

<220>
<221> modified_base
<222> (9)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (27)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (41)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (468)
<223> a, c, g, t, other or unknown
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<220>
<221> modified_base
<222> (491)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (564)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (591)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (598)
<223> a, c, g, t, other or unknown

<400> 16
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tagctgttcc ctgtgtgaaa ttgttatccg ctcacaattc cacacaacat acgagccgga 180
agcataaaagt gtaaaggctg gggtgctaa tgagttagct aactcacatt aattgcgttg 240
cgctcaactgc ccgccttcca gtcggaaac ctgtcggtcc agctgcattt atgaatcgcc 300
caacgcgcgg ggagaggcgg tttgcgtatt gggcgcttt ccgccttc gtcactgac 360
tcgctgcgtc cggtcgttcc gctgcggcgc gcggtatccat ctcactcaa ggcggtaata 420
cggttatcca cagaatcagg ggataacggg ggttaaggaca tgtggggnaa aagggcagca 480
aaagggcagg naccgtaaaa aggccgttg gttggggttt ttccataggg tccggccccc 540
tggggggat caaaaaaaaaat ccgnngccaa gtcaagggggt ggggggaccc nccagggnnt 600
ataaaaggtagc caggggttcc ccctggaggt ccctccgtgg gtctcctgtc cgccctgccc 660
gttaccgggt act
673
```